

### AMENDMENTS TO THE CLAIMS

The following listing of claims will replace all prior versions and listing of claims in the application.

1. **(currently amended)** A method for finding translation initiation codons in a nucleotide sequence, comprising:

a) analyzing a first data set to measure a combination of features of initiator codons and pseudoinitiator codons ~~[[and]]~~ to produce ~~a set of numerical values~~ scoring function parameters for said combination of features; ~~[[and]]~~

b) ~~evaluating scoring functions by~~ reading a sequence in the vicinity of an ATG triplet and using ~~[[said]]~~ one or more scoring functions and ~~[[said]]~~ one or more of the scoring ~~function's~~ function parameters to ~~return~~ determine a numerical score that quantifies how much said ATG triplet resembles an initiator codon; ~~[[and]]~~

c) using Quadratic Discriminant Analysis ~~generating a quadratic discriminant function through selection of~~ with a combination of feature variables that optimally ~~classifies~~ classify ATG triplets in a nucleotide sequence as initiator codons or as pseudoinitiator codons based on the ~~output of said scoring functions~~ numerical score determined in step b) to generate a quadratic discriminant function and through the use of Quadratic Discriminant Analysis; and

d) analyzing a second data set of nucleotide sequences using said quadratic discriminant function ~~to analyze a second data set of nucleotide sequences by~~ evaluating, wherein said analysis comprises evaluating at least one scoring function for each ATG triplet in said sequences ~~[[and]]~~ to calculate the probability whether each

ATG triplet is [[of]] an initiator codon ~~at a position using the output of said analysis;~~  
and

e) locating translation initiation codons in said second data set based on the probability calculated in step d).

2. **(original)** A method for finding translation initiation codons in a nucleotide sequence, as recited in claim 1, wherein said combination of features from step a) comprises at least two of the features provided in Table 1.

3. **(original)** A method for finding translation initiation codons in a nucleotide sequence, as recited in claim 1, wherein said scoring functions from step d) comprise at least two of the scoring functions provided in Table 2.

4. **(currently amended)** A method for finding translation initiation codons in a nucleotide sequence, as recited in claim 1, wherein said combination of feature variables from step c) comprises any combination of at least two of the feature variables provided in Table 3 wherein the combination comprises one feature variable from each of any two feature variable classes and results in a correlation coefficient for the feature variable combination **[[of]]** greater than 0.9.

5. **(currently amended)** A method for finding translation initiation codons in a nucleotide sequence, as recited in claim 1, wherein said combination of feature variables from step c) comprises any combination of at least two of the feature variables provided

in Table 3 wherein the combination comprises one feature variable from each of any two feature variable classes and results in a correlation coefficient for the feature variable combination **[[of]]** greater than 0.8.